#12
03
6/20/03

```
199 attgaggaga ggacgggcaa ggacccaagg gccctcacgg cctag              2025
202 <210> SEQ ID NO: 3
203 <211> LENGTH: 20
204 <212> TYPE: DNA
205 <213> ORGANISM: Artificial Sequence
207 <220> FEATURE:
208 <223> OTHER INFORMATION: Description of Artificial Sequence: probe or
209       primer
211 <220> FEATURE:
212 <221> NAME/KEY: tRNA
213 <222> LOCATION: (4)
214 <223> OTHER INFORMATION: w at position 4 can be T or A
216 <220> FEATURE:
217 <221> NAME/KEY: unsure
218 <222> LOCATION: (5)
219 <223> OTHER INFORMATION: s at position 5 can be C or G
221 <220> FEATURE:
222 <221> NAME/KEY: unsure
223 <222> LOCATION: (12)
224 <223> OTHER INFORMATION: s at position 12 can be C or G
226 <220> FEATURE:
227 <221> NAME/KEY: unsure
228 <222> LOCATION: (15)
229 <223> OTHER INFORMATION: r at position 15 can be G or A
231 <220> FEATURE:
232 <221> NAME/KEY: unsure
233 <222> LOCATION: (18)
234 <223> OTHER INFORMATION: y at position 18 can be T or C
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237 atcwscgacg csgartayga                                           20
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241 <211> LENGTH: 7
242 <212> TYPE: PRT
243 <213> ORGANISM: Artificial Sequence
245 <220> FEATURE:
246 <223> OTHER INFORMATION: Description of Artificial Sequence: probe or
247       primer
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250 Ile Ser Asp Ala Glu Tyr Asp
251  1             5
254 <210> SEQ ID NO: 5
255 <211> LENGTH: 20
256 <212> TYPE: DNA
257 <213> ORGANISM: Artificial Sequence
259 <220> FEATURE:
260 <223> OTHER INFORMATION: Description of Artificial Sequence: probe or
261       primer
263 <220> FEATURE:
264 <221> NAME/KEY: unsure
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Protein cannot be probe or primer

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266 <223> OTHER INFORMATION: s at position 3 can be C or G
268 <220> FEATURE:
269 <221> NAME/KEY: unsure
270 <222> LOCATION: (6)
271 <223> OTHER INFORMATION: s at position 6 can be C or G
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274 <221> NAME/KEY: unsure
275 <222> LOCATION: (8)
276 <223> OTHER INFORMATION: k at position 8 can be G or T
278 <220> FEATURE:
279 <221> NAME/KEY: unsure
280 <222> LOCATION: (9)
281 <223> OTHER INFORMATION: s at position 9 can be G or C
283 <220> FEATURE:
284 <221> NAME/KEY: unsure
285 <222> LOCATION: (12)
286 <223> OTHER INFORMATION: s at position 12 can be G or C
288 <220> FEATURE:
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290 <222> LOCATION: (15)
291 <223> OTHER INFORMATION: y at position 15 can be C or T
293 <220> FEATURE:
294 <221> NAME/KEY: unsure
295 <222> LOCATION: (18)
296 <223> OTHER INFORMATION: r at position 18 can be A or G
298 <400> SEQUENCE: 5
299 ccsgtscksc csacytgraa                                    20
302 <210> SEQ ID NO: 6
303 <211> LENGTH: 20
304 <212> TYPE: DNA
305 <213> ORGANISM: Artificial Sequence
307 <220> FEATURE:
308 <223> OTHER INFORMATION: Description of Artificial Sequence: probe or
309      primer
311 <220> FEATURE:
312 <221> NAME/KEY: unsure
313 <222> LOCATION: (9)
314 <223> OTHER INFORMATION: v at position 9 can be C, G, or A
316 <220> FEATURE:
317 <221> NAME/KEY: unsure
318 <222> LOCATION: (11)
319 <223> OTHER INFORMATION: r at position 11 can be A or G
321 <220> FEATURE:
322 <221> NAME/KEY: unsure
323 <222> LOCATION: (12)
324 <223> OTHER INFORMATION: y at position 12 can be T or C
326 <220> FEATURE:
327 <221> NAME/KEY: unsure
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                    RAW SEQUENCE LISTING ERROR SUMMARY        DATE: 05/22/2003
                    PATENT APPLICATION:  US/09/830,502A        TIME: 11:10:40

                    Input Set : A:\C26151.app
                    Output Set: N:\CRF4\05222003\I830502A.raw
```

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:15; Xaa Pos. 37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55
Seq#:15; Xaa Pos. 56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73,74
Seq#:15; Xaa Pos. 75,76,77,78,79,80,81,82,83,84,85,86,87,88,89,90,91,92,93
Seq#:15; Xaa Pos. 94,95,96,97,98,99,100,101,102,103,104,105,106,107,108,109
Seq#:15; Xaa Pos. 110,111,112,113,114,115,116,117,118,119,120,126,127,128
Seq#:15; Xaa Pos. 129,130,131,132,133,134,135,136,137,138,139,140,141,142
Seq#:15; Xaa Pos. 143,144,145,146,147,148,149,150,151,152,153,154,155,156
Seq#:15; Xaa Pos. 157,158,159,160,161,162,163,164,165,166,167,168,169,170
Seq#:15; Xaa Pos. 171,172
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Seq#:16; Xaa Pos. 37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55
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Seq#:18; Xaa Pos. 157,158,159,160,161,162,163,164,165,166,167,168,169,170
Seq#:18; Xaa Pos. 171,172
Seq#:19; Xaa Pos. 18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 05/22/2003
PATENT APPLICATION: **US/09/830,502A**   TIME: 11:10:40

Input Set : **A:\C26151.app**
Output Set: **N:\CRF4\05222003\I830502A.raw**

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Seq#:19; Xaa Pos. 129,130,131,132,133,134,135,136,137,138,139,140,141,142
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Seq#:19; Xaa Pos. 157,158,159,160,161,162,163,164,165,166,167,168,169,170
Seq#:19; Xaa Pos. 171,172
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M:341 Repeated in SeqNo=15
L:523 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:16
M:341 Repeated in SeqNo=16
L:576 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:16
M:341 Repeated in SeqNo=17
L:629 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:16
M:341 Repeated in SeqNo=18
L:682 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:16
M:341 Repeated in SeqNo=19
L:735 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:16
M:341 Repeated in SeqNo=20
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STATISTICS SUMMARY   DATE: 05/22/2003
PATENT APPLICATION: **US/10/085,418E**   TIME: 14:24:44

Input Set : **N:\jumbos\10085418\PTOMS.txt**
Output Set: **N:\CRF4\05222003\J085418E.raw**

Application Serial Number: US/10/085,418E
Alpha or Numeric or Xml: Alpha
Application Class:
Application File Date: 02-28-2002
Art Unit: OIPE
Software Application: PatentIN1.0
Total Number of Sequences: 3
Total Nucleotides: 3729
Total Amino Acids: 0
Number of Errors: 0
Number of Warnings: 0
Number of Corrections: 2

MESSAGE SUMMARY

220 C: 2 (Keyword misspelled or invalid format)

Does Not Comply
Corrected Diskette Needed
see page 4 & 6

1600

RAW SEQUENCE LISTING   DATE: 05/22/2003
PATENT APPLICATION: US/09/830,502A   TIME: 11:10:39

Input Set : **A:\C26151.app**
Output Set: **N:\CRF4\05222003\I830502A.raw**

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 3  <110> APPLICANT: Barany, Francis
 4         Cao, Weiguo
 5         Tong, Jie
 7  <120> TITLE OF INVENTION: HIGH FIDELITY THERMOSTABLE LIGASE AND USES THEREOF
 9  <130> FILE REFERENCE: 19603/2615
11  <140> CURRENT APPLICATION NUMBER: 09/830,502A
12  <141> CURRENT FILING DATE: 1999-10-29
14  <150> PRIOR APPLICATION NUMBER: 60/106,461
15  <151> PRIOR FILING DATE: 1998-10-30
17  <150> PRIOR APPLICATION NUMBER: PCT/US99/25437
18  <151> PRIOR FILING DATE: 1999-10-29
20  <160> NUMBER OF SEQ ID NOS: 20
22  <170> SOFTWARE: PatentIn Ver. 2.1
24  <210> SEQ ID NO: 1
25  <211> LENGTH: 674
26  <212> TYPE: PRT
27  <213> ORGANISM: Thermus sp.
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33  Ile Arg Tyr His Asn Tyr Leu Tyr Tyr Val Leu Asp Ala Pro Glu Ile
34              20                  25                  30
36  Ser Asp Ala Glu Tyr Asp Arg Leu Leu Arg Glu Leu Lys Glu Leu Glu
37           35                  40                  45
39  Glu Arg Phe Pro Glu Leu Lys Ser Pro Asp Ser Pro Thr Glu Gln Val
40        50                  55                  60
42  Gly Ala Arg Pro Leu Glu Ala Thr Phe Arg Pro Val Arg His Pro Thr
43   65                  70                  75                  80
45  Arg Met Tyr Ser Leu Asp Asn Ala Phe Ser Leu Asp Glu Val Arg Ala
46              85                  90                  95
48  Phe Glu Glu Arg Ile Glu Arg Ala Leu Gly Arg Lys Gly Pro Phe Leu
49             100                 105                 110
51  Tyr Thr Val Glu Arg Lys Val Asp Gly Leu Ser Val Asn Leu Tyr Tyr
52             115                 120                 125
54  Glu Glu Gly Ile Leu Val Phe Gly Ala Thr Arg Gly Asp Gly Glu Thr
55        130                 135                 140
57  Gly Glu Glu Val Thr Gln Asn Leu Leu Thr Ile Pro Thr Ile Pro Arg
58  145                 150                 155                 160
60  Arg Leu Thr Gly Val Pro Asp Arg Leu Glu Val Arg Gly Glu Val Tyr
61                 165                 170                 175
63  Met Pro Ile Glu Ala Phe Leu Arg Leu Asn Gln Glu Leu Glu Glu Ala
64             180                 185                 190
66  Gly Glu Arg Ile Phe Lys Asn Pro Arg Asn Ala Ala Ala Gly Ser Leu
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RAW SEQUENCE LISTING   DATE: 05/22/2003
PATENT APPLICATION: US/09/830,502A   TIME: 11:10:39

Input Set : A:\C26151.app
Output Set: N:\CRF4\05222003\I830502A.raw

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70     210                  215                  220
72 Phe Tyr Ala Leu Gly Leu Gly Leu Glu Glu Thr Gly Leu Lys Ser Gln
73 225                  230                  235                  240
75 His Asp Leu Leu Leu Trp Leu Arg Glu Arg Gly Phe Pro Val Glu His
76                  245                  250                  255
78 Gly Phe Thr Arg Ala Leu Gly Ala Glu Gly Val Glu Glu Val Tyr Gln
79                  260                  265                  270
81 Ala Trp Leu Lys Glu Arg Arg Lys Leu Pro Phe Glu Ala Asp Gly Val
82             275                  280                  285
84 Val Val Lys Leu Asp Asp Leu Ala Leu Trp Arg Glu Leu Gly Tyr Thr
85     290                  295                  300
87 Ala Arg Thr Pro Arg Phe Ala Leu Ala Tyr Lys Phe Pro Ala Glu Glu
88 305                  310                  315                  320
90 Lys Glu Thr Arg Leu Leu Ser Val Ala Phe Gln Val Gly Arg Thr Gly
91             325                  330                  335
93 Arg Ile Thr Pro Val Gly Val Leu Glu Pro Val Phe Ile Glu Gly Ser
94             340                  345                  350
96 Glu Val Ser Arg Val Thr Leu His Asn Glu Ser Phe Ile Glu Glu Leu
97             355                  360                  365
99 Asp Val Arg Ile Gly Asp Trp Val Leu Val His Lys Ala Gly Gly Val
100     370                  375                  380
102 Ile Pro Glu Val Leu Arg Val Leu Lys Glu Arg Arg Thr Gly Glu Glu
103 385                  390                  395                  400
105 Lys Pro Ile Ile Trp Pro Glu Asn Cys Pro Glu Cys Gly His Ala Leu
106                  405                  410                  415
108 Ile Lys Glu Gly Lys Val His Arg Cys Pro Asn Pro Leu Cys Pro Ala
109             420                  425                  430
111 Lys Arg Phe Glu Ala Ile Arg His Tyr Ala Ser Arg Lys Ala Met Asp
112     435                  440                  445
114 Ile Gln Gly Leu Gly Glu Lys Leu Ile Glu Lys Leu Leu Glu Lys Gly
115     450                  455                  460
117 Leu Val Arg Asp Val Ala Asp Leu Tyr Arg Leu Lys Lys Glu Asp Leu
118 465                  470                  475                  480
120 Val Asn Leu Glu Arg Met Gly Glu Lys Ser Ala Glu Asn Leu Leu Arg
121             485                  490                  495
123 Gln Ile Glu Glu Ser Lys Gly Arg Gly Leu Glu Arg Leu Leu Tyr Ala
124             500                  505                  510
126 Leu Gly Leu Pro Gly Val Gly Glu Val Leu Ala Arg Asn Leu Ala Leu
127     515                  520                  525
129 Arg Phe Gly His Met Asp Arg Leu Leu Glu Ala Gly Leu Glu Asp Leu
130     530                  535                  540
132 Leu Glu Val Glu Gly Val Gly Glu Leu Thr Ala Arg Ala Ile Leu Asn
133 545                  550                  555                  560
135 Thr Leu Lys Asp Pro Glu Phe Arg Asp Leu Val Arg Arg Leu Lys Glu
136             565                  570                  575
138 Ala Gly Val Glu Met Glu Ala Lys Glu Arg Glu Gly Glu Ala Leu Lys
139     580                  585                  590
```

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141 Gly Leu Thr Phe Val Ile Thr Gly Glu Leu Ser Arg Pro Arg Glu Glu
142         595             600         605
144 Val Lys Ala Leu Leu Arg Arg Leu Gly Ala Lys Val Thr Asp Ser Val
145     610             615             620
147 Ser Arg Lys Thr Ser Phe Leu Val Val Gly Glu Asn Pro Gly Ser Lys
148 625             630             635             640
150 Leu Glu Lys Ala Arg Ala Leu Gly Val Pro Thr Leu Ser Glu Glu Glu
151             645             650             655
153 Leu Tyr Arg Leu Ile Glu Glu Arg Thr Gly Lys Asp Pro Arg Ala Leu
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161 <211> LENGTH: 2025
162 <212> TYPE: DNA
163 <213> ORGANISM: Thermus sp.
165 <400> SEQUENCE: 2
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168 cttagggagc ttaaggagct ggaggagcgc tttcccgagc tcaaaagccc cgactccccc 180
169 acggaacagg tggggcgag gcctctggag gccaccttcc gcccggtgcg ccaccccacc 240
170 cgcatgtact ccctggacaa cgcctttttcc ttggacgagg tgagggcctt tgaggagcgc 300
171 atagagcggg ccctgggggcg gaaggggccc ttcctctaca ccgtggagcg caaggtggac 360
172 ggtctttccg tgaacctcta ctacgaggag ggcatcctcg tctttggggc cacccggggc 420
173 gacggggaga ccgggggagga ggtgacccag aacctcctca ccatccccac cattccccgc 480
174 cgcctcacgg gcgttccgga ccgcctcgag gtccggggcg aggtctacat gcccatagag 540
175 gccttcctca ggctcaacca ggagctggag gaggcggggg agcgcatctt caaaaacccc 600
176 aggaacgccg ccgccgggtc cttgcggcag aaagacccca gggtcacggc caggcggggc 660
177 ctgagggcca ccttttacgc cctggggctg ggcctggagg aaaccgggtt aaaaagccag 720
178 cacgaccttc tcctatggct aagagagcgg ggctttcccg tggagcacgg cttacccggg 780
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